

## SEQUENCE LISTING

```
-A-(
```

<110> Shyur, Lie-Fen
 Chen, Jui-Lin
 Yang, Ning-Sun

```
<120> A Truncated Form of Fibrobacter Succinogenes 1,3-1,4-Beta-D-Glucanase With
 Improved
      Enzymatic Activity And Thermo-Tolerance
<130> 4910-8
<140> US 09/654,652
<141> 2000-09-05
<150>
<151>
<160> 6
<210> 1
<211> 248
<212> PRT
<213> Artificial Sequence
<223> Modified enzyme with enhanced activity and thermal stability
Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
                                                          15
Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ser Gly Thr Val Ser Ser Met Phe
                 25
                                      30
                                                          35
Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu
                                      50
                                                          55
Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
                 65
                                      70
                                                          75
Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
                 85
                                      90
                                                          95
Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg
                105
                                    110
                                                         115
Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu
                125
                                     130
                                                         135
Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
                145
                                     150
                                                         155
Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser
                165
                                     170
                                                         175
                                                                              180
Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys
                185
                                    190
                                                         195
                                                                              200
Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg
                205
                                     210
                                                         215
                                                                              220
Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
                225
                                     230
                                                         235
Pro Arg Asp Asp Glu Pro Ala Pro
                245
```

```
<210> 2
```

<sup>&</sup>lt;211> 267

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Artificial Sequence

```
<223> Modified enzyme with enhanced activity and thermal stability
Met Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu Val Gln Tyr
Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser Ser Met Phe
Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val Asp Ile Glu
                                                          55
Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys Ala Gly Ala
                 65
                                      70
                                                          75
Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala Phe His Thr
                 85
                                      90
                                                          95
Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln Glu Val Arg
                105
                                     110
                                                         115
                                                                             120
Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg Phe Asn Leu
                125
                                     130
                                                         135
Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu Pro Leu Phe
                145
                                     150
                                                         155
Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu Gly Gly Ser
                165
                                     170
                                                         175
Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg Trp Gly Lys
                185
                                    190
                                                         195
                                                                             200
Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile Tyr Ser Arg
                205
                                     210
                                                         215
                                                                             220
Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn Gly Gln Val
                225
                                     230
                                                         235
                                                                             240
Pro Arg Asp Asp Glu Pro Ala Pro Asn Ser Ser Val Asp Lys Leu Ala Ala Leu
                245
                                     250
                                                         255
Glu His His His His His
                265
<210> 3
<211> 349
<212> PRT
<213> Fibrobacter succinogenes
<220>
<223>
<400> 3
Met Asn Ile Lys Lys Thr Ala Val Lys Ser Ala Leu Ala Val Ala Ala Ala Ala Ala Ala
                                                          15
Leu Thr Thr Asn Val Ser Ala Lys Asp Phe Ser Gly Ala Glu Leu Tyr Thr Leu Glu Glu
                 25
                                                          35
Val Gln Tyr Gly Lys Phe Glu Ala Arg Met Lys Met Ala Ala Ala Ser Gly Thr Val Ser
                 45
                                      50
Ser Met Phe Leu Tyr Gln Asn Gly Ser Glu Ile Ala Asp Gly Arg Pro Trp Val Glu Val
                 65
                                      70
Asp Ile Glu Val Leu Gly Lys Asn Pro Gly Ser Phe Gln Ser Asn Ile Ile Thr Gly Lys
                 85
                                      90
                                                          95
                                                                              100
Ala Gly Ala Gln Lys Thr Ser Glu Lys His His Ala Val Ser Pro Ala Ala Asp Gln Ala
                105
                                     110
                                                         115
                                                                              120
Phe His Thr Tyr Gly Leu Glu Trp Thr Pro Asn Tyr Val Arg Trp Thr Val Asp Gly Gln
                125
                                     130
                                                         135
Glu Val Arg Lys Thr Glu Gly Gly Gln Val Ser Asn Leu Thr Gly Thr Gln Gly Leu Arg
                145
                                     150
                                                         155
Phe Asn Leu Trp Ser Ser Glu Ser Ala Ala Trp Val Gly Gln Phe Asp Glu Ser Lys Leu
                165
                                    170
                                                         175
                                                                             180
Pro Leu Phe Gln Phe Ile Asn Trp Val Lys Val Tyr Lys Tyr Thr Pro Gly Gln Gly Glu
                185
                                    190
                                                         195
                                                                              200
```

260

320

```
Gly Gly Ser Asp Phe Thr Leu Asp Trp Thr Asp Asn Phe Asp Thr Phe Asp Gly Ser Arg
                205
                                    210
                                                        215
Trp Gly Lys Gly Asp Trp Thr Phe Asp Gly Asn Arg Val Asp Leu Thr Asp Lys Asn Ile
                225
                                    230
                                                        235
Tyr Ser Arg Asp Gly Met Leu Ile Leu Ala Leu Thr Arg Lys Gly Gln Glu Ser Phe Asn
                245
                                    250
                                                        255
Gly Gln Val Pro Arg Asp Asp Glu Pro Ala Pro Gln Ser Ser Ser Ala Pro Ala Ser
                265
                                    270
                                                        275
Ser Ser Val Pro Ala Ser Ser Ser Val Pro Ala Ser Ser Ser Ala Phe Val
                285
                                    290
                                                        295
Pro Pro Ser Ser Ser Ala Thr Asn Ala Ile His Gly Met Arg Thr Thr Pro Ala Val
                305
                                    310
                                                        315
Ala Lys Glu His Arg Asn Leu Val Asn Ala Lys Gly Ala Lys Val Asn Pro Asn Gly His
                325
                                    330
                                                        335
Lys Arg Tyr Arg Val Asn Phe Glu His
                345
<210> 4
<211> 744
<212> DNA
<213> Artificial Sequence
<223> Code for a modified enzyme
<400> 4
atggttagcg caaaggattt tagcggtgcc gaactctaca cgttagaaga agttcagtac 60
ggtaagtttg aagcccgtat gaagatggca gccgcatcgg gaacagtcag ttccatgttc 120
ctctaccaga atggttccga aatcgccgat ggaaggccct gggtagaagt ggatattgaa 180
gttctcggca agaatccggg cagtttccag tccaacatca ttaccggtaa ggccggcgca 240
caaaagacta gcgaaaagca ccatgctgtt agccccgccg ccgatcaggc tttccacacc 300
tacggtctcg aatggactcc gaattacgtc cgctggactg ttgacggtca ggaagtccgc 360
aagacggaag gtggccaggt ttccaacttg acaggtacac agggactccg ttttaacctt 420
tggtcgtctg agagtgcggc ttgggttggc cagttcgatg aatcaaagct tccgcttttc 480
cagttcatca actgggtcaa ggtttataag tatacgccgg gccagggcga aggcggcagc 540
gactttacgc ttgactggac cgacaatttt gacacgtttg atggctcccg ctggggcaag 600
ggtgactgga catttgacgg taaccgtgtc qacctcaccg acaagaacat ctactccaga 660
gatggcatgt tgatcctcgc cctcacccgc aaaggtcagg aaagcttcaa cggccaggtt 720
ccgagagatg acgaacctgc tccg
<210> 5
<211> 804
<212> DNA
<213> Artificial Sequence
<220>
<223> Code for a modified enzyme
<400> 5
atggttagcg caaaggattt tagcggtgcc gaactctaca cgttagaaga agttcagtac 60
ggtaagtttg aagcccgtat gaagatggca gccgcatcgg gaacagtcag ttccatgttc 120
ctctaccaga atggttccga aatcgccgat ggaaggccct gggtagaagt ggatattgaa 180
gttctcggca agaatccggg cagtttccag tccaacatca ttaccqqtaa qqccqqcqca 240
caaaagacta gegaaaagca ccatgetgtt ageceegeeg cegateagge tttecacace 300
tacggtctcg aatggactcc gaattacgtc cgctggactg ttgacggtca ggaagtccgc 360
aagacggaag gtggccaggt ttccaacttg acaggtacac agggactccg ttttaacctt 420
tggtcgtctg agagtgcggc ttgggttggc cagttcgatg aatcaaagct tccgcttttc 480
cagttcatca actgggtcaa ggtttataag tatacgccgg gccagggcga aggcggcagc 540
gactttacgc ttgactggac cgacaatttt gacacgtttg atggctcccg ctggggcaag 600
ggtgactgga catttgacgg taaccgtgtc gacctcaccg acaagaacat ctactccaga 660
gatggcatgt tgatcctcgc cctcacccgc aaaggtcagg aaagcttcaa cggccaggtt 720
```

ccgagagatg acgaacctgc tccgaattcg agctccqtcg acaagcttqc ggccqcactc 780

gagcaccacc accaccacca ctga <210> 6 <211> 1050 <212> DNA <213> Fibrobacter succinogenes <220> <223> <400> 6 atgaacatca agaaaactgc agtcaagagc gctctcgccg tagcagccgc agcagcagcc ctcaccacca atgttagcgc aaaggatttt agcggtgccg aactctacac gttagaagaa gttcagtacg gtaagtttga agcccgtatg aagatggcag ccgcatcggg aacagtcagt 180 tccatgttcc tctaccagaa tggttccgaa atcgccgatg gaaggccctg ggtagaagtg 240 gatattgaag ttctcggcaa gaatccgggc agtttccagt ccaacatcat taccggtaag 300 geoggegeae aaaagactag egaaaageae catgetgtta geoeegeege egateagget ttccacacct acggtctcga atggactccg aattacgtcc gctggactgt tgacggtcag 420 gaagtccgca agacggaagg tggccaggtt tccaacttga caggtacaca gggactccgt tttaaccttt ggtcgtctga gagtgcggct tgggttggcc agttcgatga atcaaagctt ccgcttttcc agttcatcaa ctgggtcaag gtttataagt atacgccggg ccagggcgaa ggcggcagcg actttacgct tgactggacc gacaattttg acacgtttga tggctcccgc 660 tggggcaagg gtgactggac atttgacggt aaccgtgtcg acctcaccga caagaacatc 720 tactccagag atggcatgtt gatcctcgcc ctcacccgca aaggtcagga aagcttcaac ggccaggttc cgagagatga cgaacctgct ccgcaatctt ctagcagcgc tccgqcatct tetageagtg tteeggeaag etectetage gteeetgeet eetegageag egeattigtt ccgccgagct cctcgagcgc cacaaacgca atccacggaa tgcgcacaac tccggcagtt 960 gcaaaggaac accgcaatct cgtgaacgcc aagggtgcca aggtgaaccc gaatggccac 1020 aagcgttatc gcgtgaactt tgaacactaa 1050 <210> 7 <211> 13 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 7 tcaccaccat ggttagcgca aag 13 <210> 8 <211> 15 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 8 gccacgaatt ctgttcaaag ttcac 15 <210> 9 <211> 17 <212> DNA <213> Artificial Sequence <220> <223> PCR Primer <400> 9 cagccggcga tggccatggt tagcgca

17

```
<210> 10

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 10

ctgctagaag aattcggagc aggttcgtc
```

19